

CorrectedSequenceListing-3rd.txt
SEQUENCE LISTING

<110> TAKESHIMA, Seiji
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OKA, Masanori
HIRAYAMA, Noriaki

<120> MODIFIED PYRROLOQUINOLINE QUINONE (PQQ) DEPENDENT GLUCOSE DEHYDROGENASE
EXCELLENT IN SUBSTRATE SPECIFICITY

<130> 251134

<150> PCT/JP2004/012508
<151> 2004-08-31

<150> JP 2003-315797
<151> 2003-09-08

<150> JP 2003-315799
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<150> JP 2004-060283
<151> 2004-03-04

<150> JP 2004-060282
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<150> JP 2004-151905
<151> 2004-05-21

<160> 94

<170> PatentIn version 3.1

<210> 1
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<213> Acinetobacter baumannii

<400> 1

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Phe Asp Lys Lys Val Ile Leu Ser Asn Leu Asn Lys Pro His Ala Leu
20 25 30

Leu Trp Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly
35 40 45

Lys Ile Leu Arg Val Asn Pro Val Ser Gly Ser Ala Lys Thr Val Phe
50 55 60

Gln Val Pro Glu Ile Val Ser Asp Ala Asp Gly Gln Asn Gly Leu Leu
65 70 75 80

Gly Phe Ala Phe His Pro Asp Phe Lys His Asn Pro Tyr Ile Tyr Ile

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85

90

95

Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn
 100 105 110
 Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Thr Thr Asp Thr Phe
 115 120 125
 Glu Lys Pro Ile Asp Leu Ile Ala Gly Leu Pro Ser Lys Asp His
 130 135 140
 Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
 145 150 155 160
 Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
 165 170 175
 Gln Ala Gln His Thr Pro Thr Gln Gln Glu Leu Asn Ser Lys Asp Tyr
 180 185 190
 His Thr Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Val
 195 200 205
 Pro Lys Asp Asn Pro Ser Phe Asn Gly Val Val Ser His Ile Tyr Thr
 210 215 220
 Leu Gly His Arg Asn Pro Gln Gly Leu Ala Phe Ala Pro Asn Gly Lys
 225 230 235 240
 Leu Leu Gln Ser Glu Gln Gly Pro Asn Ser Asp Asp Glu Ile Asn Leu
 245 250 255
 Val Leu Lys Gly Gly Asn Tyr Gly Trp Pro Asn Val Ala Gly Tyr Lys
 260 265 270
 Asp Asp Ser Gly Tyr Ala Tyr Ala Asn Tyr Ser Ala Ala Thr Asn Lys
 275 280 285
 Ser Gln Ile Lys Asp Leu Ala Gln Asn Gly Ile Lys Val Ala Thr Gly
 290 295 300
 Val Pro Val Thr Lys Glu Ser Glu Trp Thr Gly Lys Asn Phe Val Pro
 305 310 315 320
 Pro Leu Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp
 325 330 335

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Pro Thr Cys Gly Glu Met Ala Tyr Ile Cys Trp Pro Thr Val Ala Pro
340 345 350

Ser Ser Ala Tyr Val Tyr Thr Gly Gly Lys Lys Ala Ile Pro Gly Trp
355 360 365

Glu Asn Thr Leu Leu Val Pro Ser Leu Lys Arg Gly Val Ile Phe Arg
370 375 380

Ile Lys Leu Asp Pro Thr Tyr Ser Thr Thr Leu Asp Asp Ala Ile Pro
385 390 395 400

Met Phe Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Glu
405 410 415

Gly Asn Thr Leu Tyr Val Leu Thr Asp Thr Ala Gly Asn Val Gln Lys
420 425 430

Asp Asp Gly Ser Val Thr His Thr Leu Glu Asn Pro Gly Ser Leu Ile
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Lys Phe Thr Tyr Asn Gly Lys
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tggttaaccg aacgtgcaac tggcaaaatt ttaagagtaa atcctgtatc tggtagcgcg 180
aaaacagtat ttcaggttcc tgaaattgtg agtgatgctg atgggcaaaa tggttttgta 240
ggttttgctt ttcattcctga ctttaaaccat aacccttata tctatatattc aggcaacttt 300
aaaaatccaa aatctacaga taaagagtta cctaatacaga cgattattcg tagatatacc 360
tataataaaa ctacagatgc atttgaaaag cctattgatt tgattgcagg ttaccgtca 420
tcaaagatc atcagtcctg tcgtctcggtt attggtccag accaaaaaat ctactatacg 480
attggtgacc aaggtcgtaa tcagtttagct tatctgttct taccgaatca ggcacagcat 540
actccgactc agcaagagct caatagtaaa gactaccata catatatggg taaagtatta 600
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| aactatttcg cagcaaccaa taaatcaca attaagatt tagctcaaaa cgggataaaa | 900 |
| gtagcaacag gtgttcctgt gactaaagag tctgaatgga ctggtaaaaa ctttgtgccg | 960 |
| cctttgaaaa ctttatatac ggtacaagat acctataact ataatgacct tacttgtggt | 1020 |
| gagatggcat atatttgctg gccaacggtt gcaccgtcat cagcatatgt atatacggga | 1080 |
| ggcaaaaaa cgattccagg gtgggaaat acattattgg tcccatcttt aaaactgtgg | 1140 |
| gtgattttcc gtattaaatt ggacccgaca tatagcacga ctttggatga tgcataccca | 1200 |
| atgtttaaaa gcaataaccg ttatcgtgat gtcacgcga gtccagaagg taatacctta | 1260 |
| tatgtgctga ctgatacagc ggggaatgta caaaaagatg atggttctgt cactcatact | 1320 |
| ttagagaatc ccggttctct cattaaattt acatataacg gtaagtaa | 1368 |

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<220>
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<210> 7
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<220>
<223> Artificial Sequence oligonucleotide

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33

<210> 8
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<220>
<223> Artificial Sequence oligonucleotide

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33

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gaccaaggctc gtaatatttt agcttatctg ttc
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33

<210> 23
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<210> 24
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33

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33

<210> 26
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<400> 26
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33

<210> 27
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33

<210> 28
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<400> 28
gaacagataa gctaartgat tacgaccttg gtc
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CorrectedSequenceListing-3rd.txt

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CorrectedSequenceListing-3rd.txt

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<210> 36
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<210> 37
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<400> 37
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33

<210> 38
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<400> 38
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CorrectedSequenceListing-3rd.txt

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<210> 43
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CorrectedSequenceListing-3rd.txt

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CorrectedSequenceListing-3rd.txt

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<210> 51
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<210> 52
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<210> 54
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CorrectedSequenceListing-3rd.txt

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<210> 57
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<223> "n stands for any base"

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CorrectedSequenceListing-3rd.txt

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<210> 65
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<400> 65
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<210> 66
<211> 36
<212> DNA
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<400> 66
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<210> 67
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CorrectedSequenceListing-3rd.txt

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<210> 69
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gcttttaciaa tctgaccaag gaccaaattc tgatgatg 38

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<210> 76
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